<110> Kinney, Anthony
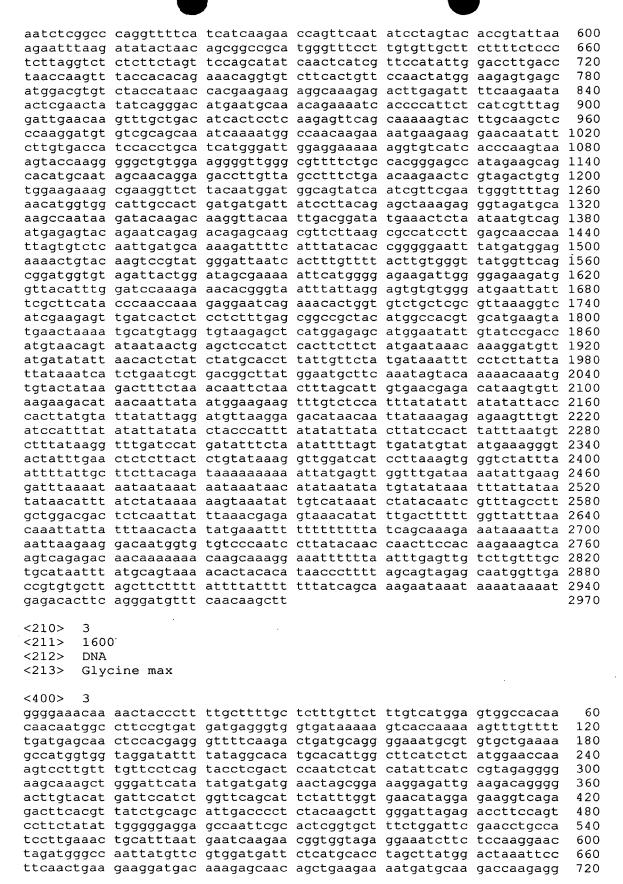
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<130> BB1432 US NA

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<150> 60/189,823
<151> 16 MARCH 2000

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<210> 1
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<212> DNA
<213> chimeric construct

<400> 1
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acaatggatg gcagtatcaa tcgttcgaat gggtttttaga acatggtggc attgccactg  660
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caaactcgta ttctcttccg ccacctcatt tttgtttatt tcaacacccg tcaaactgca  480
tgccaccccg tggccaaatg tccatgcatg ttaacaagac ctatgactat aaatatctgc  540
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agaatttaag atatactaac agcggccgca tgggtttcct tgtgttgctt cttttctccc  660
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<211>   1600
<212>   DNA
<213>   Glycine max

<400>   3
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caacaatggc cttccgtgat gatgagggtg gtgataaaaa gtcaccaaaa agtttgtttt  120
tgatgagcaa ctccacgagg gttttcaaga ctgatgcagg ggaaatgcgt gtgctgaaaa  180
gccatggtgg taggatattt tataggcaca tgcacattgg cttcatctct atggaaccaa  240
agtccttgtt tgttcctcag tacctcgact ccaatctcat catattcatc cgtagagggg  300
aagcaaagct gggattcata tatgatgatg aactagcgga aaggagattg aagacagggg  360
acttgtacat gattccatct ggttcagcat tctatttggt gaacatagga gaaggtcaga  420
gacttcacgt tatctgcagc attgacccct ctacaagctt gggattagag accttccagt  480
ccttctatat tgggggagga gccaattcgc actcggtgct ttctggattc gaacctgcca  540
tccttgaaac tgcatttaat gaatcaagaa cggtggtaga ggaaatcttc tccaaggaac  600
tagatgggcc aattatgttc gtggatgatt ctcatgcacc tagcttatgg actaaattcc  660
ttcaactgaa gaaggatgac aaagagcaac agctgaagaa aatgatgcaa gaccaagagg  720
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```
                                    2
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tctacgatga caaaaaagcc gatttcaaaa acgcttatgg ttggagcaag gcactgcatg   900
gaggcgagta tcctccactc agcgaaccgg atattggagt tttacttgtc aaactctcag   960
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caaatgctat tagaagcttt gccaatgatg tggttatgga tgttttttaa tttgaacact  1440
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<210> 4
<211> 454
<212> PRT
<213> Glycine max

<400> 4
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Leu Phe Leu Met Ser Asn Ser Thr Arg Val Phe Lys Thr Asp Ala Gly
            20                  25                  30

Glu Met Arg Val Leu Lys Ser His Gly Gly Arg Ile Phe Tyr Arg His
         35                  40                  45

Met His Ile Gly Phe Ile Ser Met Glu Pro Lys Ser Leu Phe Val Pro
    50                  55                  60

Gln Tyr Leu Asp Ser Asn Leu Ile Ile Phe Ile Arg Arg Gly Glu Ala
65                  70                  75                  80

Lys Leu Gly Phe Ile Tyr Asp Asp Glu Leu Ala Glu Arg Arg Leu Lys
            85                  90                  95

Thr Gly Asp Leu Tyr Met Ile Pro Ser Gly Ser Ala Phe Tyr Leu Val
            100                 105                 110

Asn Ile Gly Glu Gly Gln Arg Leu His Val Ile Cys Ser Ile Asp Pro
        115                 120                 125

Ser Thr Ser Leu Gly Leu Glu Thr Phe Gln Ser Phe Tyr Ile Gly Gly
    130                 135                 140

Gly Ala Asn Ser His Ser Val Leu Ser Gly Phe Glu Pro Ala Ile Leu
145                 150                 155                 160

Glu Thr Ala Phe Asn Glu Ser Arg Thr Val Val Glu Glu Ile Phe Ser
                165                 170                 175

Lys Glu Leu Asp Gly Pro Ile Met Phe Val Asp Asp Ser His Ala Pro
            180                 185                 190

Ser Leu Trp Thr Lys Phe Leu Gln Leu Lys Lys Asp Asp Lys Glu Gln
    195                 200                 205
```

3

```
Gln Leu Lys Lys Met Met Gln Asp Gln Glu Glu Asp Glu Glu Glu Lys
    210             215             220
Gln Thr Ser Arg Ser Trp Arg Lys Leu Leu Glu Thr Val Phe Gly Lys
225             230             235             240
Val Asn Glu Lys Ile Glu Asn Lys Asp Thr Ala Gly Ser Pro Ala Ser
                245             250             255
Tyr Asn Leu Tyr Asp Asp Lys Lys Ala Asp Phe Lys Asn Ala Tyr Gly
            260             265             270
Trp Ser Lys Ala Leu His Gly Gly Glu Tyr Pro Pro Leu Ser Glu Pro
        275             280             285
Asp Ile Gly Val Leu Leu Val Lys Leu Ser Ala Gly Ser Met Leu Ala
    290             295             300
Pro His Val Asn Pro Ile Ser Asp Glu Tyr Thr Ile Val Leu Ser Gly
305             310             315             320
Tyr Gly Glu Leu His Ile Gly Tyr Pro Asn Gly Ser Lys Ala Met Lys
            325             330             335
Thr Lys Ile Lys Gln Gly Asp Val Phe Val Val Pro Arg Tyr Phe Pro
            340             345             350
Phe Cys Gln Val Ala Ser Arg Asp Gly Pro Leu Glu Phe Phe Gly Phe
        355             360             365
Ser Thr Ser Ala Arg Lys Asn Lys Pro Gln Phe Leu Ala Gly Ala Ala
    370             375             380
Ser Leu Leu Arg Thr Leu Met Gly Pro Glu Leu Ser Ala Ala Phe Gly
385             390             395             400
Val Ser Glu Asp Thr Leu Arg Arg Ala Val Asp Ala Gln His Glu Ala
                405             410             415
Val Ile Leu Pro Ser Ala Trp Ala Ala Pro Pro Glu Asn Ala Gly Lys
            420             425             430
Leu Lys Met Glu Glu Glu Pro Asn Ala Ile Arg Ser Phe Ala Asn Asp
        435             440             445
Val Val Met Asp Val Phe
    450

<210>    5
<211>    494
<212>    DNA
<213>  Glycine max

<400>    5
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actgaggcaa agacttgcga gaacctggct gatacataca ggggtccatg cttcaccact   180
ggcagctgcg atgatcactg caagaacaaa gagcacttgc tcagaggcag atgcagggac   240
gattttcgct gttggtgcac caaaaactgt taaatggatc cattcactcc aacgtgaaga   300
```
4

```
agatgcatgc agcgctattt tataaaaaat acaactacta tatactatat ataataagac 360
tgggcgctgc atcaatgacc ctatgtanta tnntatatat tattaccgat gtcaagaact 420
atagatgcat gtactgtgca taacggctga gttatgtccn tangttanga ataaaaataa 480
agtgctgttg ttgc                                                    494
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```
<210>  6
<211>  75
<212>  PRT
<213>  Glycine max
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```
<400>  6
Met Glu Lys Lys Ser Ile Ala Gly Leu Cys Phe Leu Phe Leu Val Leu
 1               5                   10                  15

Phe Val Ala Gln Glu Val Val Val Gln Thr Glu Ala Lys Thr Cys Glu
            20                  25                  30

Asn Leu Ala Asp Thr Tyr Arg Gly Pro Cys Phe Thr Thr Gly Ser Cys
        35                  40                  45

Asp Asp His Cys Lys Asn Lys Glu His Leu Leu Arg Gly Arg Cys Arg
    50                  55                  60

Asp Asp Phe Arg Cys Trp Cys Thr Lys Asn Cys
65                  70                  75
```

```
<210>  7
<211>  30
<212>  DNA
<213>  Artificial Sequence
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<220>
<223>  Description of Artificial Sequence:  P34 gene primer
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<400>  7
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```
<210>  8
<211>  30
<212>  DNA
<213>  Glycine max
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```
<220>
<223>  Description of Artificial Sequence:  P34 gene primer
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<400>  8
gaattcgcgg ccgctcaaag aggagagtga                                   30
```

```
<210>  9
<211>  701
<212>  DNA
<213>  Glycine max
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atccacagcc ccaaccttct cacgtcactg ctcttattac acgacctagt tgtccggatc  180
tgagtatttg cctcaatatt ttaggcgggt ctctaggaac cgtggatgat tgttgtgccc  240
tcatcggtgg tcttggtgac attgaagcca ttgtgtgcct ttgcatccaa ctcaggccc    300
tcggaatatt aaaccttaac cgtaatttgc agttaatatt aaactcctgt ggacgaagct  360
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5

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acccgtcaaa cgccacttgc ccccgaacct aagaacagaa tatgtatggc actaattacc 420
atattacttc gtatcatggt gtttgtttgt ttgtctgtgt ttaaagttaa ggatgttata 480
cccttcgtgc ctgctacata tatatagtgg cactataat attaccaata aattaacgtc 540
catatataag aataataata aataaataaa tatttctata caaataaagg ttacgtaatg 600
ttgttgttct cgtggatggg gatcttatct tcctcctcgc tatctttgtt tatcgtattt 660
cagtgaaagt tgttcaataa aagtcctttg ttcaacaagt g                     701
```

<210> 10
<211> 119
<212> PRT
<213> Glycine max

```
<400> 10
Met Gly Ser Lys Val Val Ala Ser Val Ala Leu Leu Leu Ser Ile Asn
1               5                   10                  15

Ile Leu Phe Ile Ser Met Val Ser Ser Ser Ser His Tyr Asp Pro Gln
            20                  25                  30

Pro Gln Pro Ser His Val Thr Ala Leu Ile Thr Arg Pro Ser Cys Pro
        35                  40                  45

Asp Leu Ser Ile Cys Leu Asn Ile Leu Gly Gly Ser Leu Gly Thr Val
    50                  55                  60

Asp Asp Cys Cys Ala Leu Ile Gly Gly Leu Gly Asp Ile Glu Ala Ile
65                  70                  75                  80

Val Cys Leu Cys Ile Gln Leu Arg Ala Leu Gly Ile Leu Asn Leu Asn
                85                  90                  95

Arg Asn Leu Gln Leu Ile Leu Asn Ser Cys Gly Arg Ser Tyr Pro Ser
            100                 105                 110

Asn Ala Thr Cys Pro Arg Thr
            115
```

<210> 11
<211> 396
<212> DNA
<213> Glycine max

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actcacgctg ctatcatcgg ccaagacggc agcgtttggc ttcagagtac cgacttccct 120
cagttcaaac ctgaggagat aactgccatc atgaatgact ttaatgagcc tggatcactt 180
gctccaactg gattgtatct cggtggcacc aaatatatgg tcatccaggg tgaacccggt 240
gctgtcattc gagggaagaa gggtcctggt ggtgttactg tgaagaagac cggtgcggcc 300
ttgatcattg gcatttatga tgaaccaatg actccaggtc aatgcaacat ggtagttgaa 360
aggcttggtg attacctcat agatcaaggc tactga                           396
```

<210> 12
<211> 131
<212> PRT
<213> Glycine max

```
<400> 12
Met Ser Trp Gln Ala Tyr Val Asp Asp His Leu Leu Cys Gly Ile Glu
1               5                   10                  15
```

6

```
Gly Asn His Leu Thr His Ala Ala Ile Ile Gly Gln Asp Gly Ser Val
            20                  25                  30

Trp Leu Gln Ser Thr Asp Phe Pro Gln Phe Lys Pro Glu Glu Ile Thr
        35                  40                  45

Ala Ile Met Asn Asp Phe Asn Glu Pro Gly Ser Leu Ala Pro Thr Gly
    50                  55                  60

Leu Tyr Leu Gly Gly Thr Lys Tyr Met Val Ile Gln Gly Glu Pro Gly
65                  70                  75                  80

Ala Val Ile Arg Gly Lys Lys Gly Pro Gly Gly Val Thr Val Lys Lys
                85                  90                  95

Thr Gly Ala Ala Leu Ile Ile Gly Ile Tyr Asp Glu Pro Met Thr Pro
            100                 105                 110

Gly Gln Cys Asn Met Val Val Glu Arg Leu Gly Asp Tyr Leu Ile Asp
            115                 120                 125

Gln Gly Tyr
        130

<210>   13
<211>   396
<212>   DNA
<213>   Glycine max

<400>   13
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actcacgctg ctatcatcgg ccaagacggc agcgtttggg ctcagagtac cgacttccct 120
cagttcaaac ctgaggagat aactgccatc atgaatgact ttaatgagcc tggatcactt 180
gctccaactg gattgtatct cggtggcacc aaatatatgg tcatccaggg tgaacccggt 240
gctgtcattc gagggaagaa gggtcctggt ggtgttactg tgaagaagac cggtgcggcc 300
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aggcctggtg attacctcat cgaccagggc tactga                            396

<210>   14
<211>   131
<212>   PRT
<213>   Glycine max

<400>   14
Met Ser Trp Gln Ala Tyr Val Asp Asp His Leu Leu Cys Asp Ile Glu
1               5                   10                  15

Gly Asn His Leu Thr His Ala Ala Ile Ile Gly Gln Asp Gly Ser Val
            20                  25                  30

Trp Ala Gln Ser Thr Asp Phe Pro Gln Phe Lys Pro Glu Glu Ile Thr
        35                  40                  45

Ala Ile Met Asn Asp Phe Asn Glu Pro Gly Ser Leu Ala Pro Thr Gly
    50                  55                  60

Leu Tyr Leu Gly Gly Thr Lys Tyr Met Val Ile Gln Gly Glu Pro Gly
65                  70                  75                  80
```

```
Ala Val Ile Arg Gly Lys Lys Gly Pro Gly Gly Val Thr Val Lys Lys
            85                  90                  95

Thr Gly Ala Ala Leu Ile Ile Gly Ile Tyr Asp Glu Pro Met Thr Pro
            100                 105                 110

Gly Gln Cys Asn Met Val Val Glu Arg Pro Gly Asp Tyr Leu Ile Asp
            115                 120                 125

Gln Gly Tyr
    130


<210>   15
<211>   1746
<212>   DNA
<213>   Glycine max

<400>   15
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agagagcagc ctcagcaaaa cgagtgccag atccaaaaac tcaatgccct caaaccgggt     180
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cagtgtgccg gtgttgccct ctctcgctgc accctcaacc gcaacgccct tcgtagacct     300
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gcagtgccta ctggtgttgc atggtggatg tacaacaatg aagacactcc tgttgttgcc     540
gtttctatta ttgacaccaa cagcttggag aaccagctcg accagatgcc taggagattc     600
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caaagccaga aaggaaagca tcagcaagaa gaagaaaacg aaggaggcag catattgagt     720
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gaagaggatg agaagccaca gtgcaagggt aaagacaaac actgccaacg cccccgagga     960
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accgccacca gccttgactt cccagccctc tcgtggctca gactcagtgc tggatttggg    1140
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taccccactt ttgtcttttt ggcaatagtg ctagcaacca ataaataata ataataataa    1620
tgaataagaa aacaaaggct ttagcttgcc ttttgttcac tgtaaaataa taatgtaagt    1680
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tctgtt                                                                1746


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<211>   495
<212>   PRT
<213>   Glycine max

<400>   16
Met Ala Lys Leu Val Phe Ser Leu Cys Phe Leu Leu Phe Ser Gly Cys
1               5                   10                  15

Cys Phe Ala Phe Ser Ser Arg Glu Gln Pro Gln Gln Asn Glu Cys Gln
            20                  25                  30
```

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```
Ile Gln Lys Leu Asn Ala Leu Lys Pro Gly Asn Arg Ile Glu Ser Glu
        35                  40                  45

Gly Gly Leu Ile Glu Thr Trp Asn Pro Asn Asn Lys Pro Phe Gln Cys
        50                  55                  60

Ala Gly Val Ala Leu Ser Arg Cys Thr Leu Asn Arg Asn Ala Leu Arg
65                  70                  75                  80

Arg Pro Ser Tyr Thr Asn Gly Pro Gln Glu Ile Tyr Ile Gln Gln Gly
                85                  90                  95

Lys Gly Ile Phe Gly Met Ile Tyr Pro Gly Cys Ser Ser Thr Phe Glu
            100                 105                 110

Glu Pro Gln Gln Pro Gln Gln Arg Gly Gln Ser Ser Arg Pro Gln Asp
        115                 120                 125

Arg His Gln Lys Ile Tyr Asn Ser Arg Glu Gly Asp Leu Ile Ala Val
        130                 135                 140

Pro Thr Gly Val Ala Trp Trp Met Tyr Asn Asn Glu Asp Thr Pro Val
145                 150                 155                 160

Val Ala Val Ser Ile Ile Asp Thr Asn Ser Leu Glu Asn Gln Leu Asp
                165                 170                 175

Gln Met Pro Arg Arg Phe Tyr Leu Ala Gly Asn Gln Glu Gln Glu Phe
            180                 185                 190

Leu Lys Tyr Gln Gln Glu Gln Gly Gly His Gln Ser Gln Lys Gly Lys
        195                 200                 205

His Gln Gln Glu Glu Glu Asn Glu Gly Gly Ser Ile Leu Ser Gly Phe
        210                 215                 220

Thr Leu Glu Phe Leu Glu His Ala Phe Ser Val Asp Lys Gln Ile Ala
225                 230                 235                 240

Lys Asn Leu Gln Gly Glu Asn Glu Gly Glu Asp Lys Gly Ala Ile Val
            245                 250                 255

Thr Val Lys Gly Gly Leu Ser Val Ile Lys Pro Pro Thr Asp Glu Gln
            260                 265                 270

Gln Gln Arg Pro Gln Glu Glu Glu Glu Glu Glu Asp Glu Lys Pro
        275                 280                 285

Gln Cys Lys Gly Lys Asp Lys His Cys Gln Arg Pro Arg Gly Ser Gln
        290                 295                 300

Ser Lys Ser Arg Arg Asn Gly Ile Asp Glu Thr Ile Cys Thr Met Arg
305                 310                 315                 320

Leu Arg His Asn Ile Gly Gln Thr Ser Ser Pro Asp Ile Tyr Asn Pro
                325                 330                 335

Gln Ala Gly Ser Val Thr Thr Ala Thr Ser Leu Asp Phe Pro Ala Leu
                340                 345                 350
```

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Ser Trp Leu Arg Leu Ser Ala Gly Phe Gly Ser Leu Arg Lys Asn Ala
        355             360             365

Met Phe Val Pro His Tyr Asn Leu Asn Ala Asn Ser Ile Ile Tyr Ala
    370             375             380

Leu Asn Gly Arg Ala Leu Ile Gln Val Val Asn Cys Asn Gly Glu Arg
385             390             395             400

Val Phe Asp Gly Glu Leu Gln Glu Gly Arg Val Leu Ile Val Pro Gln
            405             410             415

Asn Phe Val Val Ala Ala Arg Ser Gln Ser Asp Asn Phe Glu Tyr Val
        420             425             430

Ser Phe Lys Thr Asn Asp Thr Pro Met Ile Gly Thr Leu Ala Gly Ala
        435             440             445

Asn Ser Leu Leu Asn Ala Leu Pro Glu Glu Val Ile Gln His Thr Phe
    450             455             460

Asn Leu Lys Ser Gln Gln Ala Arg Gln Ile Lys Asn Asn Asn Pro Phe
465             470             475             480

Lys Phe Leu Val Pro Pro Gln Glu Ser Gln Lys Arg Ala Val Ala
            485             490             495
```

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